

(1) GENERAL INFORMATION

- (2) INFORMATION FOR SEQ ID NO:1:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
1 5 10 15
Arg Pro Ala Pro
20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCTCCACCG CCCCCCAGC CCACGGTGTC ACCTCGGCCC CGGACACCAG GCCGGCCCCG 60

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Pro Asp Thr Arg Pro Ala Pro
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGCAGTACTG CACCACCGGC ACATGGCGTA ACATCAGCAC CTGATAACAAG ACCTGCACCT 60

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGATCCACCG CGCCGCCTGC GCACGGAGTG ACGTCGGCGC CCGACACGCG CCCCGCTCCC 60

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGTCAACAG CTCCTCCCGC TCATGGGGTT ACTTCTGCTC CAGATACTCG CCCAGCTCCA 60

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTTCGACGG CCCCCCTGC TCACGGTGTA ACATCCGCCC CGGATACCAG ACCGGCCCCCT 60

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCAGCACCG CACCGCCCGC ACACGGGGTC ACAAGCGCGC CAGACACTCG ACCTGCGCCA 60

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGAAGTACCG CTCCACCTGC ACACGGGGTC ACAAGCGCGC CAGACACTCG ACCTGCGCCA 60

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGTCGACTG CCCCTCCGGC GCATGGTGTG ACCTCAGCTC CTGACACAAG GCCAGCCCCA 60

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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGTTCACCG CACCTCCAGC ACACGGAGTC ACGTCTGCAC CCGACACCCG TCCAGCTCCG 60

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTAGTACAG CGCCACCCGC ACATGGCGTC ACGAGCGCTC CGGATACGAG ACCGGCGCCT 60

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGCTCCACCG CACCCCCAGC CCACGGTGTC ACCTCGGCCC CGGACACCAG GCGGGCCCCG 60
GGCTCCACCC CGGCCCCG 78

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCTCCACCG CCCCCCAGC CCATGGTGTC ACCTCGGCCC CGGACAACAG GCCCGCCTTG 60

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(2) INFORMATION FOR SEQ ID NO:16:

(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
1 5 10 15
Arg Arg Ala Pro
20

(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Asn
1 5 10 15
Arg Pro Ala Leu
20

(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Gly Ser Thr Ala Pro Pro Val His Asn Val Thr Ser Ala
1 5 10

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(A) LENGTH: 1527 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
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(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...1524
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG Met 1	ACA Thr	CCG Pro	GGC Gly	ACC Thr 5	CAG Gln	TCT Ser	CCT Pro	TTC Phe 10	TTC Phe 10	CTG Leu	CTG Leu	CTG Leu	CTC Leu	CTC Leu 15	ACA Thr	48
GTG Val	CTT Leu	ACA Thr 20	GCT Ala 20	ACC Thr	ACA Thr	GCC Ala	CCT Pro	AAA Lys 25	CCC Pro	GCA Ala	ACA Thr	GTT Val 30	GTT Val 30	ACG Thr	GGT Gly	96
TCT Ser	GGT Gly 35	CAT His 35	GCA Ala	AGC Ser	TCT Ser	ACC Thr 40	CCA Pro 40	GGT Gly	GGA Gly	GAA Glu	AAG Lys 45	GAG Glu 45	ACT Thr	TCG Ser	GCT Ala	144
ACC Thr 50	CAG Gln 50	AGA Arg	AGT Ser	TCA Ser	GTG Val	CCC Pro 55	AGC Ser 55	TCT Ser	ACT Thr	GAG Glu 60	AAG Lys 60	AAT Asn	GCT Ala	GTG Val	AGT Ser	192
ATG Met 65	ACA Thr	AGC Ser	TTG Leu	ATA Ile 70	TCG Ser 70	AAT Asn	TCC Ser	GGT Gly	GTC Val	CGG Arg 75	GGC Gly	TCC Ser	ACC Thr	GCC Ala 80	CCC Pro 80	240
CCA Pro	GCC Ala	CAC His	GGT Gly 85	GTC Val 85	ACC Thr	TCG Ser	GCC Ala	CCG Pro 90	GAC Asp 90	ACC Thr	AGG Arg	CCG Pro	GCC Ala	CCG Pro 95	GGC Gly	288
TCC Ser	ACC Thr	GCC Ala 100	CCC Pro 100	CCA Pro	GCC Ala	CAC His	GGT Gly 105	GTC Val 105	ACC Thr	TCG Ser	GCC Ala	CCG Pro	GAC Asp 110	ACC Thr	AGG Arg	336
CCG Pro	GCC Ala 115	CCG Pro 115	GGC Gly	TCC Ser	ACC Thr	GCC Ala 120	CCC Pro 120	CCA Pro	GCC Ala	CAC His	GGT Gly 125	GTC Val 125	ACC Thr	TCG Ser	GCC Ala	384
CCG Pro 130	GAC Asp 130	ACC Thr	AGG Arg	CCG Pro	GCC Ala	CCG Pro 135	GGC Gly	TCC Ser	ACC Thr	GCA Ala	CCC Pro 140	CCA Pro	GCC Ala	CAC His	GGT Gly	432
GTC Val 145	ACC Thr	TCG Ser	GCC Ala	CCG Pro	GAC Asp 150	ACC Thr	AGG Arg	CGG Arg	GCC Ala	CCG Pro 155	GGC Gly	TCC Ser	ACC Thr	CCG Pro 160	GCC Ala 160	480
CCG Pro	GGC Gly	TCC Ser	ACC Thr 165	GCC Ala 165	CCC Pro	CCA Pro	GCC Ala	CAC His	GGT Gly 170	GTC Val	ACC Thr	TCG Ser	GCC Ala	CCG Pro 175	GAC Asp	528
ACC Thr	AGG Arg	CCG Pro 180	GCC Ala 180	CCG Pro	GGC Gly	TCC Ser	ACC Thr 185	GCC Ala 185	CCC Pro	CCA Pro	GCC Ala	CAT His 190	GGT Gly 190	GTC Val	ACC Thr	576
TCG Ser	GCC Ala 195	CCG Pro 195	GAC Asp	AAC Asn	AGG Arg	CCC Pro 200	GCC Ala 200	TTG Leu	GGC Gly	TCC Ser	ACC Thr 205	GCC Ala 205	CCT Pro	CCA Pro	GTC Val	624

CAC His	AAT Asn	GTC Val	ACC Thr	TCG Ser	GCC Ala	TCA Ser	GGC Gly	TCT Ser	GCA Ala	TCA Ser	GGC Gly	TCA Ser	GCT Ala	TCT Ser	ACT Thr	672
210						215					220					
CTG Leu	GTG Val	CAC His	AAC Asn	GGC Gly	ACC Thr	TCT Ser	GCC Ala	AGG Arg	GCT Ala	ACC Thr	ACA Thr	ACC Thr	CCA Pro	GCC Ala	AGC Ser	720
225					230					235					240	
AAG Lys	AGC Ser	ACT Thr	CCA Pro	TTC Phe	TCA Ser	ATT Ile	CCC Pro	AGC Ser	CAC His	CAC His	TCT Ser	GAT Asp	ACT Thr	CCT Pro	ACC Thr	768
				245					250					255		
ACC Thr	CTT Leu	GCC Ala	AGC Ser	CAT His	AGC Ser	ACC Thr	AAG Lys	ACT Thr	GAT Asp	GCC Ala	AGT Ser	AGC Ser	ACT Thr	CAC His	CAT His	816
			260					265					270			
AGC Ser	ACG Thr	GTA Val	CCT Pro	CCT Pro	CTC Leu	ACC Thr	TCC Ser	TCC Ser	AAT Asn	CAC His	AGC Ser	ACT Thr	TCT Ser	CCC Pro	CAG Gln	864
		275					280					285				
TTG Leu	TCT Ser	ACT Thr	GGG Gly	GTC Val	TCT Ser	TTC Phe	TTT Phe	TTC Phe	CTG Leu	TCT Ser	TTT Phe	CAC His	ATT Ile	TCA Ser	AAC Asn	912
	290					295					300					
CTC Leu	CAG Gln	TTT Phe	CCT Pro	TCC Ser	TCT Ser	CTC Leu	GAA Glu	GAT Asp	CCC Pro	AGC Ser	ACC Thr	GAC Asp	TAC Tyr	TAC Tyr	CAA Gln	960
305					310					315					320	
GAG Glu	CTG Leu	CAG Gln	AGA Arg	GAC Asp	ATT Ile	TCT Ser	CAA Gln	ATG Met	TTT Phe	TTG Leu	CAG Gln	ATT Ile	TAT Tyr	AAA Lys	CAA Gln	1008
				325					330					335		
GGG Gly	GGT Gly	TTT Phe	CTG Leu	GGC Gly	CTC Leu	TCC Ser	AAT Asn	ATT Ile	AAG Lys	TTC Phe	AGG Arg	CCA Pro	GGA Gly	TCT Ser	GTG Val	1056
			340					345					350			
CTG Leu	GTA Val	CAA Gln	TTG Leu	ACT Thr	CTG Leu	GCC Ala	TTC Phe	CGA Arg	GAA Glu	GGT Gly	ACC Thr	ATC Ile	AAT Asn	GTC Val	CAC His	1104
		355					360					365				
GAC Asp	GTG Val	GAG Glu	ACA Thr	CAG Gln	TTC Phe	AAT Asn	CAG Gln	TAT Tyr	AAA Lys	ACG Thr	GAA Glu	GCA Ala	GCC Ala	TCT Ser	CGA Arg	1152
	370					375					380					
TAT Tyr	AAC Asn	CTG Leu	ACG Thr	ATC Ile	CCA Pro	GAC Asp	GTC Val	AGC Ser	GTG Val	AGT Ser	GAT Asp	GTG Val	CCA Pro	TTT Phe	CCT Pro	1200
385					390					395					400	
TTC Phe	TCT Ser	GCC Ala	CAG Gln	TCT Ser	GGG Gly	GCT Ala	GGG Gly	GTG Val	CCA Pro	GGC Gly	TGG Trp	GGC Gly	ATC Ile	GCG Ala	CTG Leu	1248
				405				410						415		
CTC Leu	CTG Leu	CTG Leu	GTC Val	TGT Cys	GTT Val	CTG Leu	GTT Val	GCG Ala	CTG Leu	GCC Ala	ATT Ile	GTC Val	TAT Tyr	CTC Leu	ATT Ile	1296
			420					425					430			
GCC Ala	TTG Leu	GCT Ala	GTC Val	TGT Cys	CAG Gln	TGC Cys	CGC Arg	CGA Arg	AAG Lys	AAC Asn	TAC Tyr	GGG Gly	CAG Gln	CTG Leu	GAC Asp	1344
		435					440					445				

ATC TTT CCA GCC CGG GAT ACC TAC CAT CCT ATG AGC GAG TAC CCC ACC	1392
Ile Phe Pro Ala Arg Asp Thr Tyr His Pro Met Ser Glu Tyr Pro Thr	
450 455 460	
TAC CAC ACC CAT GGG CGC TAT GTC CCC CCT AGC AGT ACC GAT CGT AGC	1440
Tyr His Thr His Gly Arg Tyr Val Pro Pro Ser Ser Thr Asp Arg Ser	
465 470 475 480	
CCC TAT GAG AAG GTT TCT GCA GGT AAT GGT GGC AGC AGC CTC TCT TAC	1488
Pro Tyr Glu Lys Val Ser Ala Gly Asn Gly Gly Ser Ser Leu Ser Tyr	
485 490 495	
ACA AAC CCA GCA GTG GCA GCC ACT TCT GCC AAC TTG TAG	1527
Thr Asn Pro Ala Val Ala Ala Thr Ser Ala Asn Leu	
500 505	

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr	1 5 10 15
Val Leu Thr Ala Thr Thr Ala Pro Lys Pro Ala Thr Val Val Thr Gly	20 25 30
Ser Gly His Ala Ser Ser Thr Pro Gly Gly Glu Lys Glu Thr Ser Ala	35 40 45
Thr Gln Arg Ser Ser Val Pro Ser Ser Thr Glu Lys Asn Ala Val Ser	50 55 60
Met Thr Ser Leu Ile Ser Asn Ser Gly Val Arg Gly Ser Thr Ala Pro	65 70 75 80
Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly	85 90 95
Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg	100 105 110
Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala	115 120 125
Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly	130 135 140
Val Thr Ser Ala Pro Asp Thr Arg Arg Ala Pro Gly Ser Thr Pro Ala	145 150 155 160
Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp	165 170 175
Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr	180 185 190
Ser Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser Thr Ala Pro Pro Val	195 200 205
His Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser Ala Ser Thr	210 215 220
Leu Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr Pro Ala Ser	225 230 235 240
Lys Ser Thr Pro Phe Ser Ile Pro Ser His His Ser Asp Thr Pro Thr	

				245				250				255			
Thr	Leu	Ala	Ser	His	Ser	Thr	Lys	Thr	Asp	Ala	Ser	Ser	Thr	His	His
				260					265				270		
Ser	Thr	Val	Pro	Pro	Leu	Thr	Ser	Ser	Asn	His	Ser	Thr	Ser	Pro	Gln
				275					280				285		
Leu	Ser	Thr	Gly	Val	Ser	Phe	Phe	Phe	Leu	Ser	Phe	His	Ile	Ser	Asn
				290					295				300		
Leu	Gln	Phe	Pro	Ser	Ser	Leu	Glu	Asp	Pro	Ser	Thr	Asp	Tyr	Tyr	Gln
305						310					315				320
Glu	Leu	Gln	Arg	Asp	Ile	Ser	Gln	Met	Phe	Leu	Gln	Ile	Tyr	Lys	Gln
				325						330					335
Gly	Gly	Phe	Leu	Gly	Leu	Ser	Asn	Ile	Lys	Phe	Arg	Pro	Gly	Ser	Val
				340					345				350		
Leu	Val	Gln	Leu	Thr	Leu	Ala	Phe	Arg	Glu	Gly	Thr	Ile	Asn	Val	His
				355				360					365		
Asp	Val	Glu	Thr	Gln	Phe	Asn	Gln	Tyr	Lys	Thr	Glu	Ala	Ala	Ser	Arg
						375						380			
Tyr	Asn	Leu	Thr	Ile	Pro	Asp	Val	Ser	Val	Ser	Asp	Val	Pro	Phe	Pro
385					390						395				400
Phe	Ser	Ala	Gln	Ser	Gly	Ala	Gly	Val	Pro	Gly	Trp	Gly	Ile	Ala	Leu
				405						410					415
Leu	Leu	Leu	Val	Cys	Val	Leu	Val	Ala	Leu	Ala	Ile	Val	Tyr	Leu	Ile
				420				425					430		
Ala	Leu	Ala	Val	Cys	Gln	Cys	Arg	Arg	Lys	Asn	Tyr	Gly	Gln	Leu	Asp
				435				440				445			
Ile	Phe	Pro	Ala	Arg	Asp	Thr	Tyr	His	Pro	Met	Ser	Glu	Tyr	Pro	Thr
						455						460			
Tyr	His	Thr	His	Gly	Arg	Tyr	Val	Pro	Pro	Ser	Ser	Thr	Asp	Arg	Ser
465					470						475				480
Pro	Tyr	Glu	Lys	Val	Ser	Ala	Gly	Asn	Gly	Gly	Ser	Ser	Leu	Ser	Tyr
				485						490					495
Thr	Asn	Pro	Ala	Val	Ala	Ala	Thr	Ser	Ala	Asn	Leu				
				500					505						